

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 7, 2002, 16:05:25 ; Search time 77.81 Seconds

(Without alignments)
22,618 Million cell updates/sec

Title: US-08-569-749-9

Perfect score: 295
Sequence: -1 PEQLASAGFYVGRNDVK.....CWESGDPPWEHAKWPRCE 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	295	100.0	618 1	BIR3_HUMAN
2	290	98.3	611 1	BIR_CHICK
3	282	95.6	358 1	PIAP_PIG
4	282	95.6	604 1	BIR2_HUMAN
5	282	95.6	612 1	BIR3_MOUSE
6	268	90.8	600 1	BIR2_MOUSE
7	198	67.1	268 1	IAP3_NPYOP
8	187	63.4	1403 1	BIRF_MOUSE
9	186	63.1	1402 1	BIRG_MOUSE
10	186	63.1	1403 1	BIRA_MOUSE
11	186	63.1	1403 1	BIRE_MOUSE
12	183	62.0	1447 1	BIRB_MOUSE
13	182	61.7	275 1	IAP_GVCP
14	178	60.3	1403 1	BIR1_HUMAN
15	174	59.0	496 1	BIR4_MOUSE
16	174	59.0	496 1	BIR4_MOUSE
17	174	59.0	497 1	BIR4_MOUSE
18	160	54.2	438 1	BIR4_MOUSE
19	156	52.9	498 1	IAP2_DROME
20	118	40.0	286 1	IAP1_NPYAC
21	117.5	39.8	4828 1	BIR6_HUMAN
22	110	37.6	273 1	IAP1_NPYOP
23	110	37.6	273 1	IAP1_NPYOP
24	104	35.3	939 1	ZEP_TYRV
25	90.5	30.7	140 1	BIR1_SCHPO
26	90.5	30.7	140 1	BIR5_MOUSE
27	87.5	29.7	142 1	BIR5_MOUSE
28	87.5	29.7	142 1	BIR5_MOUSE
29	65.5	22.9	224 1	IAPL_ASFB7
30	61.5	20.8	224 1	IAPL_ASFB7
31	61.5	20.8	224 1	IAPL_ASFB7
32	61.5	20.8	224 1	IAPL_ASFB7
33	58.5	19.8	1173 1	TSP1_XENLA

34	58	19.7	556 1	NUMB_DROME	P16554 drosophila
35	57.5	19.5	156 1	BDP_HUMAN	P36639 homo sapien
36	57.5	19.5	555 1	HYDL_STRHA	O05355 streptomyce
37	57.5	19.3	1004 1	POIL_SCTCO	O03277 sclera copr
38	56	19.0	65 1	MTR_STRPU	O27287 strongyloce
39	55.5	18.8	1536 1	SIN3_YEAST	P22579 saccharomyc
40	55	18.6	92 1	PMG_AYATH	O02973 arabidopsis
41	55	18.6	954 1	BIR1_YEAST	P47134 saccharomyc
42	54.5	18.5	249 1	IAP2_NPYAC	P41454 autographa
43	54.5	18.5	347 1	CAR1_EPHMO	P18956 ephydella m
44	54.5	18.5	1170 1	TSP1_BOVIN	O28178 bos taurus
45	54.5	18.5	1170 1	TSP1_HUMAN	P07996 homo sapien

ALIGNMENTS

RESULT ID	1	STANDARD:	PRT:	618 AA.
BIR3_HUMAN				
AC	Q13490: Q16516;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS PROTEIN 2) (HIAP2) (HIAP-2) (C-IAP1) (TNFR2-TNFR SIGNALING COMPLEX PROTEIN 2) (IAP HOMOLOG B).			
DE	PROTEIN 2) (IAP HOMOLOG B).			
GN	BIRC3 OR AIP2 OR IAP2 OR MIBB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
NP	[1]			
NP	SEQUENCE FROM N.A.			
RX	MDLINP-96128127; PubMed-8548910;			
RA	Reche M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;			
RT	"The TNFR2-TNFR signaling complex contains two novel proteins related to baculoviral inhibitor of apoptosis proteins.";			
RL	Cell 83:1243-1252(1995).			
NP	[2]			
NP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MDLINP-9614949; PubMed-8552191;			
RA	Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertton-Horvat G.,			
RA	Farbman R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;			
RT	"Suppression of apoptosis in mammalian cells by NAIP and a related family of IAP genes.";			
RL	Nature 379:349-353(1996).			
NP	[3]			
NP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal Liver;			
RX	MDLINP-96209843; PubMed-8643514;			
RA	Uren A.G., Pakusch M., Hawkins C.J., Puls K.D., Vaux D.L.;			
RT	"Cloning and expression of apoptosis inhibitor protein homologs that function to inhibit apoptosis and/or bind tumor necrosis factor receptor-associated factors.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).			
NP	[4]			
NP	STRUCTURE BY NMR OF 266-363			
RX	MDLINP-99332054; PubMed-10404221;			
RA	Hinds M.G., Norton R.S., Vaux D.L., Day C.L.;			
RT	"Solution structure of a baculoviral inhibitor of apoptosis (IAP) repeat.";			
RL	Nat. Struct. Biol. 6:648-651(1999).			
CC	-1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).			
CC	-1- TISSUE SPECIFICITY: PRESENT IN MANY FETAL AND ADULT TISSUES.			
CC	MAINTAINED IN ADULT SKELETAL MUSCLE, THYMUS, TESTIS, OVARY, AND PANCREAS. LOW OR ABSENT IN BRAIN AND PERIPHERAL BLOOD LEUCOCYTES.			

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CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: I49431; AAC1942.1; -
DR EMBL: U45879; AAC50372.1; -
DR EMBL: U37547; AAC50508.1; -
DR PDB: 10BH; 20-OCT-99.
DR MM: 601721; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR Apoptosis: Zinc-finger; Repeat: 3D-structure.
DR REPEAT 46 113 BIR 1.
DR REPEAT 184 250 BIR 2.
DR REPEAT 269 336 BIR 3.
DR DOMAIN 453 539 CARD.
DR 2N_FING 571 605 RING-TYPE.
DR CONFLICT 157 157 S -> P (IN REF. 2).
DR CONFLICT 308 308 C -> G (IN REF. 2).
DR CONFLICT 414 414 Q -> L (IN REF. 2).
DR CONFLICT 514 514 L -> W (IN REF. 2).
DR SEQUENCE 618 AA; 69899 MW; C1778D328065586D CRC64;
SO
Query Match 100.0%; Score 295; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 4.4e-29;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PEOLASAGFYVGRNDYKCFCCDGLRCWESGDDPWVWHAHAKMPFCE 48
DB 287 PEOLASAGFYVGRNDYKCFCCDGLRCWESGDDPWVWHAHAKMPFCE 334
RESULT 2
BIR_CHICK STANDARD; PRT; 611 AA.
ID BIR_CHICK
AC Q90660;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE INHIBITOR OF APOPTOSIS PROTEIN (IAP) (INHIBITOR OF T CELL APOPTOSIS
DE PROTEIN).
GN ITA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Splice.
RX MEDLINE=97101113; PubMed=8945639;
RA Diggby M.R., Kimpson W.G., York J.J., Connick T.E., Lowenthal J.W.;
RA ITA, a vertebrate homologue of IAP that is expressed in T
RT

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RT lymphocytes."
RL DNA Cell Biol. 15:981-988(1996).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY NUCLEAR.
CC -1- TISSUE SPECIFICITY: CELLS OF THE T LYMPHOCYTE LINEAGE. FOUND IN
CC BOTH CORTICAL AND MEDULLARY CELLS OF THE THYMUS.
CC -1- DEVELOPMENTAL STAGE: HIGH LEVELS ARE INDUCED WITHIN 4-6 HOURS OF
CC T-CELL ACTIVATION IN SPLEEN AND THYMUS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U37466; AAB48118.1; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; ZnF_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00114; CARD; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS0209; CARD; 1.
DR Apoptosis: Zinc-finger; Repeat: Nuclear protein.
DR REPEAT 30 97 BIR 1.
DR REPEAT 176 242 BIR 2.
DR REPEAT 262 329 BIR 3.
DR 2N_FING 564 598 RING-TYPE.
DR SEQUENCE 611 AA; 69009 MW; 53FC9136F34EBDD CRC64;
SO
Query Match 98.3%; Score 290; DB 1; Length 611;
Best Local Similarity 95.8%; Pred. No. 1.8e-28;
Matches 46; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 PEOLASAGFYVGRNDYKCFCCDGLRCWESGDDPWVWHAHAKMPFCE 48
DB 280 PEOLASAGFYVGRNDYKCFCCDGLRCWESGDDPWVWHAHAKMPFCE 327
RESULT 3
PIAP_PIG STANDARD; PRT; 358 AA.
ID PIAP_PIG
AC O62640;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE INHIBITOR OF APOPTOSIS.
GN PIAP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=96073;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=98162622; PubMed=9510111;
RX Stehlik C., de Martin R., Binder B.R., Lipp J.;
RA "Cytokine induced expression of porcine inhibitor of apoptosis
RA protein (Iap) family member is regulated by NF-kappa B.";
RA Biochem. Biophys. Res. Commun. 243:827-832(1998).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.

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CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U79143; AAC39171.1; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 2.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00238; Zf-C3HC4; 1.
DR SMART: SM00238; BIR; 2.
DR SMART: SM00184; CARD; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 2.
DR PROSITE: PS0143; BIR_REPEAT_2; 2.
DR PROSITE: PS50209; CARD; 1.
DR Apoptosis; Zinc-finger; Repeat.
FT REPEAT 4 70 BIR 1.
FT REPEAT 90 157 BIR 2.
FT ZN_FING 311 345 RING-TYPE.
SQ SEQUENCE 358 AA; 40977 MW; EB2268FA9A6190A4 CRC64;

Query Match 95.6%; Score 282; DB 1; Length 358;
Best Local Similarity 93.8%; Pred. No. 1,1e-27;
Matches 45; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 PEOLASGEFYVGRNDVCKFCDCDGLRCWESGDDPWYEAHAKPFRC 48
Db 108 PEOLASGEFYVGRNDVCKFCDCDGLRCWESGDDPWYEAHAKPFRC 155
|||||
ID BIR2_HUMAN STANDARD; PRT; 604 AA.
AC 013489; 016628; 090P46;
DT 01-NOV-1997 (Ref. 35, Last sequence update)
DT 01-NOV-1997 (Ref. 35, Last annotation update)
DT 20-MAY-2002 (Ref. 40, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN (INHIBITOR OF APOPTOSIS
DE PROTEIN 1) (HIAPI) (HIAPI-1) (C-1AP2) (TNFR2-TRAF SIGNALING COMPLEX
DE PROTEIN 1) (IAP HOMOLOG C).
GN BIRC2 OR API1 OR IAP1 OR MING.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-96128127; PubMed-8548910;
RX Rothe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TRAF signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins";
RL Cell 83:1243-1252(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE-96149249; PubMed-8552191;
RX Liston P., Roy N., Tamai K., Lefebvre C., Baird S., Chertion-Horvat G.,
RX Farhan R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.;
RT "Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes";
RL Nature 379:349-353(1996).
RN (3)

RP SEQUENCE FROM N.A.
RC TISSUE=Rectal Liver;
RX MEDLINE-96209843; PubMed-8643514;
RX Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT "Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN (4)
RP SEQUENCE FROM N.A.
RX MEDLINE-99252096; PubMed-10233894;
RX Horvets A.J., Fontijn R.D., van Zonneveld A.J., de Vries C.J.,
RX ten Cate J.M., Pannekoek H.;
RT "Vascular endothelial genes that are responsive to tumor necrosis
RT factor-alpha in vitro are expressed in atherosclerotic lesions,
RT including inhibitor of apoptosis protein-1, stannin, and two novel
RT genes";
RL Blood 93:3418-3431(1999).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH THE RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL LUNG, AND KIDNEY. IN
CC THE ADULT, EXPRESSION IS MAINLY SEEN IN LYMPHOID TISSUES,
CC INCLUDING SPLEEN, THYMUS AND PERIPHERAL BLOOD LYMPHOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: L49432; AAC41943.1; -
DR EMBL: 045878; AAC50371.1; -
DR EMBL: 037546; AAC50507.1; -
DR EMBL: AF070674; AAC83232.1; -
DR MIM: 601712; -
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00653; BIR; 3.
DR Pfam: PF00619; CARD; 1.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00238; BIR; 3.
DR SMART: SM00184; CARD; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS0143; BIR_REPEAT_2; 3.
DR PROSITE: PS50209; CARD; 1.
KW Apoptosis; Zinc-finger; Repeat.
FT REPEAT 29 96 BIR 1.
FT REPEAT 169 235 BIR 2.
FT REPEAT 255 322 BIR 3.
FT DOMAIN 447 525 CARD.
FT ZN_FING 557 591 RING-TYPE.
FT CONFLICT 118 119 N -> Y (IN REF. 4).
FT CONFLICT 153 153 D -> H (IN REF. 2).
FT CONFLICT 163 163 H -> P (IN REF. 2).
FT CONFLICT 165 165 A -> P (IN REF. 2).
FT CONFLICT 191 191 K -> R (IN REF. 2).
FT CONFLICT 364 364 F -> L (IN REF. 2).
FT CONFLICT 552 552 Q -> P (IN REF. 2).
SQ SEQUENCE 604 AA; 68371 MW; 8581A0BA9A4A4A7 CRC64;

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Oy      1  PGLASAGFYVGRNDVKRCFCDCGLRCWESGDDPVVHAKKFPCE 48
Db      273 PGLASAGFYVGRNDVKRCFCDCGLRCWESGDDPVVHAKKFPCE 320

RESULT 5
BIR3_MOUSE STANDARD: PRT: 612 AA.
AC Q02210; 008864;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-APR-2001 (Rel. 40, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 3 (INHIBITOR OF APOPTOSIS
DE PROTEIN 2) (MIAP2) (MIAP-2).
DE BIRC3 OR API2 OR IAP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RA MEDLINE=966128127; PubMed=8548810;
RT Rodhe M., Pan M.-G., Henzel W.J., Ayres T.M., Goeddel D.V.;
RT "The TNFR2-TNFR1 signaling complex contains two novel proteins related
RT to baculoviral inhibitor of apoptosis proteins."
RL Cell 83:1243-1252(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=skeletal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RX Liston P., Lefebvre C., Fong W.G., Xuan J.Y., Korneluk R.G.;
RT "Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes."
RL Genomics 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: CYTOSOLSMIC (POTENTIAL).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, SPLEEN, LUNG,
CC LIVER, SKELETAL MUSCLE, KIDNEY, AND TESTIS.
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC -----
DR EMBL: LA9433; AAC42078.1; -
DR EMBL: U88909; AAC53532.1; -
DR MGD: MGI:1197009; Birc3.
DR InterPro: IPR001370; BIR.
DR InterPro: IPR001315; CARD.
DR Pfam: PF00653; BIR: 3
DR Pfam: PF00653; CARD: 1
DR Pfam: PF00653; ZF-CINC4; 1.
DR SMART: SM00238; BIR: 3.
DR SMART: SM00114; CARD: 1.
DR SMART: SM00184; RING: 1.
DR PROSITE: PS01282; BIR_REPEAT_1; 3.
DR PROSITE: PS50143; BIR_REPEAT_2; 3.
DR PROSITE: PS50149; CARD: 1.

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KW APOPTOSIS: ZINC-FINGER REPEAT. BIR. 1.
FT REPEAT 46 113 BIR. 2.
FT REPEAT 177 243 BIR. 3.
FT REPEAT 262 329 CARD.
FT DOMAIN 447 533 CARD.
FT ZNF.FING 565 599 RING-TYPE.
FT CONFLICT 380 380 E->K (IN REF. 2)
SQ SEQUENCE 612 AA: 69676 MW: E08969D3C6C610D CRC64:

Query Match 95.68; Score 282; DB 1; Length 612;
Best Local Similarity 93.88; Pred. No. 1.8e-27;
Matches 45; Conservative 1; Mismatches 2; Indels 0; Gaps 0.

QY 1 PEQLASAGFYVGRNDIVKCFCCDGGTLRWESGDDPWEHAKWPRCE 48
Db 280 PEQLASAGFYVGRNDIVKCFCCDGGTLRWESGDDPWEHAKWPRCE 327
|||||
BIR2_MOUSE 6
BIR2_MOUSE STANDARD; PRT: 600 AA.
ID BIR2_MOUSE
AC 00863;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 2 (INHIBITOR OF APOPTOSIS
DE PROTEIN 1) (MIAP) (MIAP-1).
DE BIRC2 OR API1 OR IAP1.
GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090.
RN R1 SEQUENCE FROM N.A.
RC TISSUE=skelatal muscle;
RX MEDLINE=98110590; PubMed=9441758;
RA Liston P., Delcambre C., Fong W.G., Xuan Y.Y., Korneluk R.G.;
RT Genomic characterization of the mouse inhibitor of apoptosis protein
RT 1 and 2 genes.
RL Genomids 46:495-503(1997).
CC -1- FUNCTION: APOPTOTIC SUPPRESSOR. THE BIR MOTIFS REGION INTERACTS
CC WITH TNF RECEPTOR ASSOCIATED FACTORS 1 AND 2 (TRAF1 AND TRAF2) TO
CC FORM AN HETEROOMERIC COMPLEX, WHICH IS THEN RECRUITED TO THE TUMOR
CC NECROSIS FACTOR RECEPTOR 2 (TNFR2) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOSOLSMC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE IAP FAMILY.
CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
CC -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: U88908; AAC53531.1; -.
CC MGD: MGI:1197007; B1RC2.
CC InterPro: IPR001370; BIR.
CC InterPro: IPR001315; CARD.
CC InterPro: IPR001841; znf_ring.
CC Pfam: PF00653; BIR. 3.
CC Pfam: PF00619; CARD. 1.
CC Pfam: PF00097; ZF-CRHC4; 1.
CC SMART: SM00238; BIR. 3.
CC SMART: SM00114; CARD. 1.
CC SMART: SM0184; RING. 1.
CC PROSITE: PS01282; BIR_REPEAT_1; 3.
CC PROSITE: PS50143; BIR_REPEAT_2; 3.
CC PROSITE: PS50209; CARD; 1.

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KW Apoptosis: Zinc-finger; Repeat.
 FT REPEAT 27 94 BIR 1.
 FT REPEAT 167 233 BIR 2.
 FT REPEAT 253 320 BIR 3.
 FT DOMAIN 444 512 CARD.
 FT ZN_FING 553 587 RING-TYPE.
 SO SEQUENCE 600 AA: 67198 MW: AD7F73E6849317D1 CRC64:

Query Match 90.8%; Score 268; DB 1; Length 600;
 Best Local Similarity 89.4%; Pred. No. 9, 2e-26;
 Matches 42; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 EQLASAGFYVGRNDYKFCDCDGLRCWESGDDPWVERHAKMFPRCE 48
 DB 272 DELASAGFYTGSHSDYKFCDCDGLRCWESGDDPWVERHAKMFPRCE 318

RESULT 7
 ID IAP3_NPVOP STANDARD: PRT: 268 AA.
 AC P41437.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE APOPTOSIS INHIBITOR 3 (IAP-3).
 GN IAP3 OR IAP.
 OS Oryzias pseudotsugata multicapsid polyhedrosis virus (OpkNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolydnavirus.
 OX NCBI_Taxid=164623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94187094; PubMed=8139034.
 RA Birnbaum M.J., Clem R.J., Miller L.K.;
 RT "An apoptosis-inhibiting gene from a nuclear polyhedrosis virus
 RT encoding a polypeptide with Cys/His sequence motifs."
 RL J. Virol. 68:2521-2528(1994).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97271300; PubMed=9126251;
 RA Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
 RA Kohmann G.F.;
 RT "The sequence of the Oryzias pseudotsugata multicapsid nuclear
 RT polyhedrosis virus genome."
 RL Virology 229:381-399(1997).
 CC -1- FUNCTION: ACTS BY BLOCKING CELLULAR APOPTOSIS RATHER THAN BY
 CC PREVENTING VIRAL STIMULATION OF APOPTOSIS.
 CC -1- SIMILARITY: CONTAINS 2 BIR REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC -----
 CC EMBL: L22564; AAB02610.1;
 DR EMBL: U75930; AAC59034.1;
 DR InterPro: IPR001370; BIR.
 DR InterPro: IPR001841; znf_fing.
 DR Pfam: PF00653; BIR. 2.
 DR Pfam: PF00097; zf-C3HC4. 1.
 DR SMART: SM00238; BIR. 2.
 DR SMART: SM00184; RING. 1.
 DR PROSITE: PS01287; BIR_REPEAT_1; 2.
 DR PROSITE: PS0143; BIR_REPEAT_2; 2.
 KW Apoptosis; Zinc-finger; Repeat;
 FT REPEAT 18 94 BIR 1.
 FT REPEAT 111 178 BIR 2.
 FT ZN_FING 221 255 RING-TYPE.

SO SEQUENCE 268 AA: 30076 MW: DF89175FDE85A708 CRC64:

Query Match 67.1%; Score 198; DB 1; Length 268;
 Best Local Similarity 60.4%; Pred. No. 1, 9e-17;
 Matches 29; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 1 PEGLASAGFYVGRNDYKFCDCDGLRCWESGDDPWVERHAKMFPRCE 48
 DB 129 PERLASAGFYTGCGDKTRCCDGLKDWEDDAPWQGHARWYDRCE 176

RESULT 8
 ID BIRF_MOUSE STANDARD: PRT: 1403 AA.
 AC Q9JRG6; P91704; O09122; O09121;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN IF (NEURONAL APOPTOSIS
 DE INHIBITORY PROTEIN 6).
 GN BIRCIP OR NAIP6 OR NAIP-RS4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20414747; PubMed=10958627;
 RA Estrizzi M.G., Hadinoto V., Growney J.D., Miller W., Dietrich W.F.;
 RT "Genomic sequence analysis of the mouse Naip gene array."
 RL Genome Res. 10:1095-1102(2000).
 RL [2]
 RP SEQUENCE OF 82-168 FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=97131520; PubMed=8975718;
 RA Schart J.M., Damron D., Frisella A., Bruno S., Beggs A.H.,
 RA Kunkel L.W., Dietrich W.F.;
 RT "The mouse region syntenic for human spinal muscular atrophy lies
 RT within the 1qnl critical interval and contains multiple copies of Naip
 RT exon 5."
 RL Genomics 38:405-417(1996).
 RL CC -1- FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
 CC SIGNALS.
 CC -1- SIMILARITY: CONTAINS 3 BIR REPEATS.
 CC -----
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 CC -----
 CC EMBL: AF242431; AAF82751.1;
 DR EMBL: U63427; AAC52875.1;
 DR MGI: MGI:1298422; Birc1f.
 DR InterPro: IPR001370; BIR.
 DR Pfam: PF00653; BIR. 3.
 DR SMART: SM00238; BIR. 3.
 DR PROSITE: PS01282; BIR_REPEAT_1; 2.
 DR PROSITE: PS0143; BIR_REPEAT_2; 3.
 KW Apoptosis; Repeat; Multigene family.
 FT REPEAT 60 127 BIR 1.
 FT REPEAT 159 227 BIR 2.
 FT REPEAT 278 345 BIR 3.
 SO SEQUENCE 1403 AA: 159823 MW: 9D4912503358C4E9 CRC64:

Query Match 63.4%; Score 187; DB 1; Length 1403;
 Best Local Similarity 60.4%; Pred. No. 2e-15;
 Matches 29; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

RP FUNCTION.
RC TISSUE-Liver;
RA MEDLINE-96149249; PubMed-8552191;
RX Liston P., Roy N., Tamai K., LeFebvre C., Baird S., Chertton-Horvat G.,
RA Parahani R., McLean M., Ikeda J., Mackenzie A., Korneluk R.G.,
RT Suppression of apoptosis in mammalian cells by NAIP and a related
RT family of IAP genes.
RL Nature 379:349-353(1996).
CC - FUNCTION: PREVENTS MOTOR-NEURON APOPTOSIS INDUCED BY A VARIETY OF
CC SIGNALS.
CC - TISSUE SPECIFICITY: EXPRESSED IN MOTOR NEURONS, BUT NOT IN SENSORY
CC NEURONS. FOUND IN LIVER AND PLACENTA, AND IN A LESSER EXTENT IN
CC SPINAL CORD.
CC - DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN
CC INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE 1). SMAS
CC ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE 1
CC (MERONIG-HOEFMANN DISEASE), TYPE II (INTERMEDIATE FORM), AND TYPE
CC III (WOLFF-PARK-KUENSELBERG-MELANDER DISEASE) BASED UPON THE AGE OF
CC ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE
CC CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO
CC PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
CC MEMBERS.
CC - SIMILARITY: CONTAINS 3 BIR REPEATS.
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CC
CC EMBL: U19251; AAC52045.1;
CC EMBL: U80017; AAC52047.1;
CC EMBL: U21913; AAA64504.1;
CC EMBL: AC005031; AAC62261.1;
CC MIM: 600335;
CC InterPro: IPR001370; BIR.
CC Pfam: PF00653; BIR; 3.
CC SMART: SMO0238; BIR; 3.
CC PROSITE: PS01282; BIR-REPEAT_1; 3.
CC PROSITE: PS50143; BIR-REPEAT_2; 3.
CC KW Apoptosis; Repeat.
CC FT REPEAT 60 127 BIR 1.
CC FT REPEAT 159 227 BIR 2.
CC FT REPEAT 278 345 BIR 3.
CC FT CONFLICT 222 223 PK->YR (IN REF. 4).
CC FT CONFLICT 386 387 VP->ST (IN REF. 3).
CC FT CONFLICT 535 535 M->V (IN REF. 3).
CC FT CONFLICT 553 553 Y->H (IN REF. 3).
CC FT CONFLICT 1228 1231 MISSING (IN REF. 4).
CC FT SEQUENCE 1403 AA; 159613 MW; 566304C154DA5E64 CRC64;
SQ
Query Match 60.3%; Score 178; DB 1; Length 1403;
Best Local Similarity 60.4%; Pred. No. 2; Le-14;
Matches 29; Conservative 5; Mismatches 14; Indels 0; Gaps 0;
OY 1 PEOLASAGFYVGRNDVYKFCDDGLRCWESGDDPWVEMHAKWPPRCE 48
DB 178 PCVLSAAGFYVGRNDVYKFCDDGLRCWESGDDPWVEMHAKWPPRCE 225
RESULT 15
BIR4_MOUSE
ID BIR4_MOUSE STANDARD: PRT: 496 AA.
AC 060989; 008865;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 4 (INHIBITOR OF APOPTOSIS
DE PROTEIN 3) (X-LINKED INHIBITOR OF APOPTOSIS PROTEIN) (X-LINKED IAP)
DE (IAP HOMOLOG A) (MIAP3) (MIAP-3).

GN BIRCA OR API3 OR XIAP OR AIP4 OR MIHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI-Taxid-10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X CBA; TISSUE-Liver;
RX MEDLINE-96209843; PubMed-8643514;
RX Uren A.G., Pakusch M., Hawkins C.J., Puls K.L., Vaux D.L.;
RT Cloning and expression of apoptosis inhibitory protein homologs that
RT function to inhibit apoptosis and/or bind tumor necrosis factor
RT receptor-associated factors.
RL Proc. Natl. Acad. Sci. U.S.A. 93:4974-4978(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Parahani R., LeFebvre C., Korneluk R.G., Mackenzie A.E.;
RL Submitted (JUN-1997) to the EMBL/Genbank/DBJ databases.
CC - FUNCTION: APOPTOTIC SUPPRESSOR. INHIBITOR OF CASPASE-3 AND
CC CASPASE-7 (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC - SIMILARITY: BELONGS TO THE IAP FAMILY.
CC - SIMILARITY: CONTAINS 3 BIR REPEATS.
CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC
CC EMBL: U36842; AAC52594.1;
CC EMBL: U88990; AAB5876.1;
CC MGD: MG1:107372; BIRCA.
CC InterPro: IPR001370; BIR.
CC Pfam: PF00653; BIR; 3.
CC SMART: SMO0238; BIR; 3.
CC PROSITE: PS01282; BIR-REPEAT_1; 3.
CC PROSITE: PS50143; BIR-REPEAT_2; 3.
CC KW Apoptosis; Zinc-finger; Repeat.
CC FT REPEAT 26 93 BIR 1.
CC FT REPEAT 163 230 BIR 2.
CC FT REPEAT 264 329 BIR 3.
CC FT ZN-FING 449 483 RING-TYPE.
CC FT CONFLICT 208 208 E->K (IN REF. 2).
CC FT CONFLICT 317 317 E->D (IN REF. 2).
CC FT CONFLICT 322 322 W->C (IN REF. 2).
CC FT CONFLICT 346 346 S->P (IN REF. 2).
CC FT CONFLICT 360 360 S->P (IN REF. 2).
CC FT CONFLICT 388 388 I->L (IN REF. 2).
CC FT CONFLICT 449 449 C->S (IN REF. 2).
CC FT CONFLICT 462 462 V->F (IN REF. 2).
CC FT CONFLICT 468 468 V->A (IN REF. 2).
CC FT CONFLICT 490 490 K->N (IN REF. 2).
CC FT SEQUENCE 496 AA; 56079 MW; EC5FAE0799F2CDD8 CRC64;
SQ
Query Match 59.0%; Score 174; DB 1; Length 496;
Best Local Similarity 59.6%; Pred. No. 3; Le-14;
Matches 28; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
OY 2 EQLASAGFYVGRNDVYKFCDDGLRCWESGDDPWVEMHAKWPPRCE 48
DB 281 EQLASAGFYVGRNDVYKFCDDGLRCWESGDDPWVEMHAKWPPRCE 327
Search completed: January 7, 2002, 16:05:26

Tue Jan 8 08:24:00 2002

Job time: 1405 sec

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